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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/847,010

DATE: 05/15/2001
TIME: 15:18:15

Input Set : A:\Frey.app
Output Set: N:\CRF3\05152001\I847010.raw

3 <110> APPLICANT: FREY, Perry A.
4 RUZICKA, Frank J.
6 <120> TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
8 <130> FILE REFERENCE: 032026/0476
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/847,010
C--> 11 <141> CURRENT FILING DATE: 2001-05-01
13 <150> PRIOR APPLICATION NUMBER: US 09/198,942
14 <151> PRIOR FILING DATE: 1998-11-24
16 <160> NUMBER OF SEQ ID NOS: 32
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1251
22 <212> TYPE: DNA
23 <213> ORGANISM: Clostridium subterminale
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1248)
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32 1 5 10 15
34 tgg aat gac tgg aga tgg caa gta aga aac aga ata gaa act gtt gaa 96
35 Trp Asn Asp Trp Arg Trp Gln Val Arg Asn Arg Ile Glu Thr Val Glu
36 20 25 30
38 gaa cta aag aaa tac ata cca tta aca aaa gaa gaa gaa gga gta 144
39 Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Gly Val
40 35 40 45
42 gct caa tgt gta aaa tca tta aga atg gct att act cca tat tat cta 192
43 Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu
44 50 55 60
46 tca tta atc gat cct aac gat cct aat gat cca gta aga aaa caa gct 240
47 Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala
48 65 70 75 80
50 att cca aca gca tta gag ctt aac aaa gct gct gca gat ctt gaa gac 288
51 Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp
52 85 90 95
54 cca tta cat gaa gat aca gat tca cca gta cct gga tta act cac aga 336
55 Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg
56 100 105 110
58 tat cca gat aga gta tta tta ata act gat atg tgc tca atg tac 384
59 Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
60 115 120 125
62 tgc aga cac tgt aca aga aga aga ttt gca gga caa agc gat gac tct 432
63 Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser
64 130 135 140
66 atg cca atg gaa aga ata gat aaa gct ata gat tat atc aga aat act 480
67 Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr

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68	145	150	155	160	
70	cct caa gtt aga gac gta tta tca ggt gga gac gct ctt tta gta				528
71	Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val				
72	165	170	175		
74	tct gat gaa aca tta gaa tac atc ata gct aaa tta aga gaa ata cca				576
75	Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro				
76	180	185	190		
78	cac gtt gaa ata gta aga ata ggt tca aga act cca gtt gtt ctt cca				624
79	His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro				
80	195	200	205		
82	caa aga ata act cca gaa ctt gta aat atg ctt aaa aaa tat cat cca				672
83	Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro				
84	210	215	220		
86	gta tgg tta aac act cac ttt aac cat cca aat gaa ata aca gaa gaa				720
87	Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu				
88	225	230	235	240	
90	tca act aga gct tgt caa tta ctt gct gac gca gga gta cct cta gga				768
91	Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly				
92	245	250	255		
94	aac caa tca gtt tta tta aga gga gtt aac gat tgc gta cac gta atg				816
95	Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met				
96	260	265	270		
98	aaa gaa tta gtt aac aaa tta gta aaa ata aga gta aga cct tac tac				864
99	Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr				
100	275	280	285		
102	atc tat caa tgt gac tta tca tta gga ctt gag cac ttc aga act cca				912
103	Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro				
104	290	295	300		
106	gtt tct aaa ggt atc gaa atc att gaa gga tta aga gga cat act tca				960
107	Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser				
108	305	310	315	320	
110	gga tac tgc gta cca aca ttc gtt gac gct cca ggt ggt ggt gga				1008
111	Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly				
112	325	330	335		
114	aaa aca cca gtt atg cca aac tac gtt att tca caa agt cat gac aaa				1056
115	Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys				
116	340	345	350		
118	gta ata tta aga aac ttt gaa ggt gtt ata aca act tat tca gaa cca				1104
119	Val Ile Leu Arg Asn Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro				
120	355	360	365		
122	ata aac tat act cca gga tgc aac tgt gat gtt tgc act ggc aag aaa				1152
123	Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys				
124	370	375	380		
126	aaa gtt cat aag gtt gga gtt gct gga tta tta aac gga gaa gga atg				1200
127	Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met				
128	385	390	395	400	
130	gct cta gaa cca gta gga tta gag aga aat aag aga cac gtt caa gaa				1248
131	Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln Glu				
132	405	410	415		

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Input Set : A:\Frey.app
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134 taa 1251
 137 <210> SEQ ID NO: 2
 138 <211> LENGTH: 416
 139 <212> TYPE: PRT
 140 <213> ORGANISM: Clostridium subterminale
 142 <400> SEQUENCE: 2
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 144 Trp Asn Asp Trp Arg Trp Gln Val Arg Asn Arg Ile Glu Thr Val Glu
 146 20 25 30
 147 Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Gly Val
 149 35 40 45
 150 Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu
 152 50 55 60
 153 Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala
 155 65 70 75 80
 156 Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp
 158 85 90 95
 159 Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg
 161 100 105 110
 162 Tyr Pro Asp Arg Val Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
 164 115 120 125
 165 Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser
 167 130 135 140
 168 Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr
 170 145 150 155 160
 171 Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val
 173 165 170 175
 174 Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro
 176 180 185 190
 177 His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro
 179 195 200 205
 180 Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro
 182 210 215 220
 183 Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu
 185 225 230 235 240
 186 Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly
 188 245 250 255
 189 Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met
 191 260 265 270
 192 Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr
 194 275 280 285
 195 Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro
 197 290 295 300
 198 Val Ser Lys Gly Ile Glu Ile Glu Gly Leu Arg Gly His Thr Ser
 200 305 310 315 320
 201 Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly Gly
 203 325 330 335
 204 Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys

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Input Set : A:\Frey.app
Output Set: N:\CRF3\05152001\I847010.raw

207	340	345	350
209 Val Ile Leu Arg Asn Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro			
210 355	360	365	
212 Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys			
213 370	375	380	
215 Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met			
216 385	390	395	400
218 Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln Glu			
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222 <210> SEQ ID NO: 3			
223 <211> LENGTH: 1029			
224 <212> TYPE: DNA			
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227 <220> FEATURE:			
228 <221> NAME/KEY: CDS			
229 <222> LOCATION: (1)...(1026)			
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234 1 5 10 15			
236 acg caa ctt gcc gat gtt gtg acc gat cct gat gaa ctt ctg cgt ctt	96		
237 Thr Gln Leu Ala Asp Val Val Thr Asp Pro Asp Glu Leu Leu Arg Leu			
238 20 25 30			
240 ttg aat ata gac gcg gag gaa aaa ctg tta gcc gga cgc agc gcc aaa	144		
241 Leu Asn Ile Asp Ala Glu Glu Lys Leu Ala Gly Arg Ser Ala Lys			
242 35 40 45			
244 aag ctt ttt gcc ctg cgt gtg ccc cgc tca ttt atc gat cgc atg gag	192		
245 Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu			
246 50 55 60			
248 aaa ggc aat ccg gac gat cct ctt ttg cgt cag gta ctt acc tcg caa	240		
249 Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln			
250 65 70 75 80			
252 gat gag ttt gtc atc gcg ccc gga ttc tcc acc gac cca ctg gaa gaa	288		
253 Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu			
254 85 90 95			
256 cag cac agc gta gtg cct ggt ttg ttg cat aaa tac cac aac cgg gcg	336		
257 Gln His Ser Val Val Pro Gly Leu Leu His Lys Tyr His Asn Arg Ala			
258 100 105 110			
260 ctt ttg ctg gtc aaa ggc ggc tgc gcg gta aat tgc cgc tat tgc ttc	384		
261 Leu Leu Val Lys Gly Gly Ala Val Asn Cys Arg Tyr Cys Phe			
262 115 120 125			
264 cgt cgt cac ttc ccc tat gcc gaa aat cag ggc aac aag cgt aac tgg	432		
265 Arg Arg His Phe Pro Tyr Ala Glu Asn Gln Gly Asn Lys Arg Asn Trp			
266 130 135 140			
268 caa act gca ctt gag tat gtt gct gcg cat ccg gaa ctg gac gag atg	480		
269 Gln Thr Ala Leu Glu Tyr Val Ala Ala His Pro Glu Leu Asp Glu Met			
270 145 150 155 160			
272 att ttc tcc ggc ggc gat ccg ctg atg gcg aaa gat cac gag ctg gac	528		
273 Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu Asp			

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274	165	170	175	
276	tgg ttg ctc aca caa ctg gaa gcc atc ccg cat ata aaa cgt ctg cg	576		
277	Trp Leu Leu Thr Gln Leu Glu Ala Ile Pro His Ile Lys Arg Leu Arg			
278	180	185	190	
280	att cac agc cgt ctg ccg att gtg atc ccg gca cgt atc acc gag g	624		
281	Ile His Ser Arg Leu Pro Ile Val Ile Pro Ala Arg Ile Thr Glu Ala			
282	195	200	205	
284	ctg gtt gaa tgc ttt gcc cgt tct acg ctg caa atc ttg ctg gtg aat	672		
285	Leu Val Glu Cys Phe Ala Arg Ser Thr Leu Gln Ile Leu Leu Val Asn			
286	210	215	220	
288	cac atc aac cat gcc aat gag gta gat gaa aca ttc cgt cag g	720		
289	His Ile Asn His Ala Asn Glu Val Asp Glu Thr Phe Arg Gln Ala Met			
290	225	230	235	240
292	gct aag ttg cgc cgg gta ggc gtt act ttg ctg aac cag agc gtt ctg	768		
293	Ala Lys Leu Arg Arg Val Gly Val Thr Leu Leu Asn Gln Ser Val Leu			
294	245	250	255	
296	tta cgt gat gtg aac gat aac gca caa acg ctg gca aac ctg agt aat	816		
297	Leu Arg Asp Val Asn Asp Asn Ala Gln Thr Leu Ala Asn Leu Ser Asn			
298	260	265	270	
300	gcg ttg ttc gat gcc ggc gta atg ccg tat tac ctg cat gtg ctc gat	864		
301	Ala Leu Phe Asp Ala Gly Val Met Pro Tyr Tyr Leu His Val Leu Asp			
302	275	280	285	
304	aaa gta cag ggc gcg gcg cat ttt atg gtg agt gat gac gaa gca cgg	912		
305	Lys Val Gln Gly Ala Ala His Phe Met Val Ser Asp Asp Glu Ala Arg			
306	290	295	300	
308	cag att atg cgt gag ttg ctg aca ctg gtg tcg gga tat ctg gtg ccg	960		
309	Gln Ile Met Arg Glu Leu Leu Thr Leu Val Ser Gly Tyr Leu Val Pro			
310	305	310	315	320
312	aaa ctg gcg cga gaa att ggc ggc gaa ccc agc aaa acg ccg ctg gat	1008		
313	Lys Leu Ala Arg Glu Ile Gly Gly Glu Pro Ser Lys Thr Pro Leu Asp			
314	325	330	335	
316	ctc cag cta cgc cag cag taa			1029
317	Leu Gln Leu Arg Gln Gln			
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322	<211> LENGTH: 342			
323	<212> TYPE: PRT			
324	<213> ORGANISM: Escherichia coli			
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330	Thr Gln Leu Ala Asp Val Val Thr Asp Pro Asp Glu Leu Leu Arg Leu			
331	20	25	30	
333	Leu Asn Ile Asp Ala Glu Glu Lys Leu Leu Ala Gly Arg Ser Ala Lys			
334	35	40	45	
336	Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu			
337	50	55	60	
339	Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln			
340	65	70	75	80

Please Note:

Use f n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is present in the <220> to <223> fields of each sequence which presents at least one non-r Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/847,010

DATE: 05/15/2001
TIME: 15:18:16

Input Set : A:\Frey.app
Output Set: N:\CRF3\05152001\I847010.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20